

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 523 bits (1346), Expect = 6e-146

Identities = 262/398 (65%), Positives = 313/398 (78%), Gaps = 1/398 (0%)

Query	371	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDRVVTYNALINAFVKEGKFFEAEEL	430
		P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVALLDRLMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	431	YDEMLPRGII-PNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSNLTITNTLIDGYC	489
		+M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	490	GAKRIDDGMELLHEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIV	549
		+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISPDRVTFSGSLINALVKEGDLNSAQDLLQEMISSGVCPNVV	183
Query	550	TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDLDAHPFNGVEPDVQTYNILISGLINEGK	609
		TC+TLLDGLCD GKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYNILISGLINEGK	
Sbjct	184	TCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK	243
Query	610	FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTT	669
		FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T	
Sbjct	244	FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT	303
Query	670	LINGYCKAGRVDGGLFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG	729
		LI GYCKAG VDDGGLFCEMGRRGIVANAITYITLI GFRKVGNGING+LDIFQEMISSG	
Sbjct	304	LITGYCKAGMVDGGLFCEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG	363
Query	730	VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYY 767	
		VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSMV +	
Sbjct	364	VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVSF 401	

Score = 394 bits (1012), Expect = 3e-107

Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query	263	CRPNVVTFTTLMNGLCREGRIVEAVALLDRLMEDGLQPTQITYGTIVDGMCKKGDTVSAL	322
		C+PNVVTFTTLMNGLCREGR+VEAVALLDRLM+EDGLQP QITYGTIVDGMCK GDTVSAL	
Sbjct	2	CKPNVVTFTTLMNGLCREGRVVEAVALLDRLMVEDGLQPNQITYGTIVDGMCKMGDTVSAL	61
Query	323	NLLRKMEEVSHIIPNVVIYSAIIDLCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVG	382
		NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G	
Sbjct	62	NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING	121
Query	383	FCSSGRWSDAEQLLQEMLERKISPDRVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPN	442
		FCSSG+WS+A++LLQEML RKISPDRVVT++ LINA VKEG A++L EM+ G+ PN	
Sbjct	122	FCSSGKWSEAQRLLQEMLVRKISPDRVTFSGSLINALVKEGDLNSAQDLLQEMISSGVCPN	181

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Query  443  TITYSSMIDGFCKQNRLDAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA  491
          +T ++++DG C + +L  A  MF  M              A  G  P++ T+N LI G
Sbjct  182  VVTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMMDIDATHAFNGVEPDVQTYNIIISGLINE  241

Query  492  KRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTC  551
          +  +  EL  EM   G+V DT TY+++I+G          L+ A  +   M S   P+IVT
Sbjct  242  GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF  301

Query  552  DTLLDGLCDNGKLDKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNIIISGLINEGKFL  611
          +TL+ G C  G + D LE+F  M +              G+  +  TY  LI G   G
Sbjct  302  NTLITGYCKAGMVDDGLELFCCEMGR-----RGIVANAITYITLIRGFRKVGNNIN  350

Query  612  EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM  655
          + ++++EM   G+ PDTIT  +M+ GL  +  L  A  M  +  +
Sbjct  351  GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL  394

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Score = 300 bits (767), Expect = 8e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

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Query  230  PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVAL  289
          P+VVTFTTL++GLC E RV EA+   +M E   +PN +T+ T+++G+C+ G  V A+ L
Sbjct   4   PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  290  LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIDSL  348
          L +M E   ++P  + Y  I+DG+ K G   A NL  +M++  I P++V YS +I+
Sbjct  64   LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF  122

Query  349  CKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLQEMLE-----  401
          C  G+ S+AQ L  EM  + I PD+ T++ +I          G  + A+ LLQEM+
Sbjct  123  CSSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV  182

Query  402  -----RKISPDPVVTYNALINAFVKEG  422
          + PDV TYN LI+  + EG
Sbjct  183  VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMMDIDATHAFNGVEPDVQTYNIIISGLINEG  242

Query  423  KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFN  482
          KF EAEELY+EM  RGI+P+T+TYSSMI+G CKQ+RLD A  MF  M +K  SPN++TFN
Sbjct  243  KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN  302

Query  483  TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAAALDLLQEMISS  542
          TLI GYC A  +DDG+EL  EM   G+VA+  TY TLI GF  VG++N +LD+ QEMISS
Sbjct  303  TLITGYCKAGMVDDGLELFCCEMGRRGIVANAITYITLIRGFRKVGNNINGSLDIFQEMISS  362

Query  543  GLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQKS  577
          G+ PD +T   +L GL   +LK AL M  +  +Q S
Sbjct  363  GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS  397

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## Group 5

Score = 216 bits (551), Expect = 8e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query	160	PSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALST	219
		P+VV F LM + R R ++L +M ++ + ++ ++ C AL+	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVAL LDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	220	FGKITKL G-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLC	278
		K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	279	REGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV	338
		G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISP DVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVC PN	182
Query	339	VIYSAIIDS LCKDGRHSDAQNLFTMQE-----KGIFPDLFTYNSMIVGFCSSG	387
		V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G	
Sbjct	183	VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG	242
Query	388	RWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIPNTITYS	447
		++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++	
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN	302
Query	448	SMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDGMEELLHEMTET	507
		++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +	
Sbjct	303	TLITGYCKAGMVDDGLELFC EMGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS	362
Query	508	GLVADTTTTYNTLIHGFYLVGDLNAALDLLQEM	539
		G+ DT T ++ G + +L AL +L+E+	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 193 bits (491), Expect = 8e-47

Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	145	DAIDLFS DMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMER-KQIRCDIYSFNIL	203
		+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +	
Sbjct	24	EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAI	83
Query	204	IKFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC	263
		I + A + F ++ G+ PD+VT++ +++G C + SEA +M	
Sbjct	84	IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI	143
Query	264	RPNVVTFTTLMNGLCREGRIVEAVAL LDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	323
		P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL	
Sbjct	144	SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC PNVTTCNTLLDGLCDRGKLDKDALE	203
Query	324	LLRKME-----EVSH----IIPNVVIYSAIIDS LCKDGRHSDAQNLFTMQEKGIFPDL	373
		+ + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD	
Sbjct	204	MFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMPHRGIVPDT	263

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Query  374  FTYNMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEELYDE  433
          TY+SMI G C   R  +A Q+   M  +  SP++VT+N LI  + K G   +  EL+ E
Sbjct  264  VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCE  323

Query  434  MLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR  493
          M  RGI+ N ITY ++I GF K   ++ +  +F M + G  P+ IT   ++ G   +
Sbjct  324  MGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE  383

Query  494  IDDGMELLHEM   504
          +   +  +L E+
Sbjct  384  LKRALAMLEEL   394

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Score = 118 bits (296), Expect = 3e-24  
Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

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Query  135  SGFHEIKGLEDAIDLFSDDLRSRPLPSVVDFFCKLMGVVVRMERPDLVISLYQKMERKQIR  194
          +GF      +A L  +ML  +  P VV F  L+  +V+   +   L Q+M   +
Sbjct  120  NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC  179

Query  195  CDIYSFNILIKFCSCSKLPFALSTFGKITKL-----GLHPDVVTFTTLLHGLC  243
          ++ + N L+   C   KL  AL  F  + K               G+ PDV T+  L+ GL
Sbjct  180  PNVVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI  239

Query  244  VEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI  303
          E +  EA + + +M      P+ VT+++++NGLC++ R+ EA  + D M      P  +
Sbjct  240  NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIV  299

Query  304  TYGTIVDGMCKKGDTVSAIINLLRKMEEVSHIIPNVVIYSAIIDSCLKDGRHSDAQNLFTE  363
          T+ T++ G CK G      L L  +M      I+ N + Y  +I   K G  + + ++F E
Sbjct  300  TFNTLITGYCKAGMVDDGLELFCEMGRRG-IVANAITYITLIRGFRKVGNGINGSLDIFQE  358

Query  364  MQEKGIFPDLFTYNMIVGFCSSGRWSDAEQLLQEMLERKIS   405
          M  G++PD T  +M+ G  S      A  +L+E+   +S
Sbjct  359  MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS   400

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- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

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- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

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- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSYSYEIK	60
Query	142	GLEDAIDLFSMDLRSLRPLPSVVDVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	201
		GLEDAIDLFSMDLRSLRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSMDLRSLRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120
Query	202	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFET	261
		ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFTTLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFTTLLHGLCLDHRVSEALDLFHQI---	177
Query	262	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRLMEDGLQPTQITYGTIVDGMCKKGDTVSA	321
		CRP+V+TFTTLMNGLCREGR+VEAVALLDRLM+E+GLQP QITYGT VDG MCK GDTVSA	
Sbjct	178	-CRPDVLTFTTLMNGLCREGRVVEAVALLDRLMVENGLQPDQITYGTIVDGMCKMGDTVSA	236

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Query	322	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIV	381
Sbjct	237	LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	382	GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFCISGRWSAAQRLQEMLERKISPNVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL	501
Sbjct	357	NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL	416
Query	502	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTCDTLLDGLCDN	561
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	562	GKLKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP	621
Sbjct	477	GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTF TTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	596
Query	682	DGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	741
Sbjct	597	DGLELFCCEMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEKLQMSMVY	766
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+ Y	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1624 bits (4206), Expect = 0.0

Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGSSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Sbjct	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGSSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Query	61	LADSSRVFFRDRRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFRDRRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120

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Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD L	180
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD L	180
Query	181	VISLYQKMERKQIRCDIYSFNILIKCFSCSKLPFALSTFGKITKLGLHPDVVTFTTLLH	240
Sbjct	181	VISLYQKMERKQIRCDIYSFNILIKCFSCSKLPFALSTFGKITKLGLHPDVVTFTTLLH	240
Query	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Sbjct	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNL	360
Sbjct	301	TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNL	360
Query	361	FTEMQEKGIFPD LFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	420
Sbjct	361	FTEMQEKGIFPD LFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	420
Query	421	EGKFFEAEEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPLIT	480
Sbjct	421	EGKFFEAEEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPLIT	480
Query	481	FNTLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMI	540
Sbjct	481	FNTLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMI	540
Query	541	SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYN IL	600
Sbjct	541	SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYN IL	600
Query	601	ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	660
Sbjct	601	ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	660
Query	661	SPNVVTFTTLINGYCKAGRVDDGLELFCEMGRRGIVANAITYITL ICGFRKVG NINGALD	720
Sbjct	661	SPNVVTFTTLINGYCKAGRVDDGLELFCEMGRRGIVANAITYITL ICGFRKVG NINGALD	720
Query	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMS MVYYWSELKRHTFQKIS	780
Sbjct	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMS MVYYWSELKRHTFQKIS	780
Query	781	GVKRCLGVCPFC SCHHGYRQARSS	804
Sbjct	781	GVKRCLGVCPFC SCHHGYRQARSS	804

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)**



## Group 5

Score = 975 bits (2521), Expect = 0.0

Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	144	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	203
		EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVID FCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	204	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF T TLLHGLCVEDRVSEALDFFHQMFETTC	263
		+KCFCSKLPFALSTFGKITKLGL FH	
Sbjct	120	MKCFCSKLPFALSTFGKITKLGL-----FH-----	145
Query	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFTSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA	200
Query	324	LLRKMEEVSHIIPNVVIYS AIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	377
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	378	SMIVGFCSSGRWSDAEQLLQEMLERK-ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	436
		MI GFCSSGRWS+A+QLLQEMLERK ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQQLLQEMLERKKISP DVVTYNALINAFVKEGKFFAEELYDEMLP	319
Query	437	RGIIPNTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	496
		RGIIP+TITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPIITFNTLIAGYCRAKRVDD	379
Query	497	GMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	556
		G++LLHEMTE GLVA+T TY TLIHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHGFCQVGD LNAAQDLLQEMVSSGVC PNVVTCNTLLD	439
Query	557	GLCDNGKLKDALEMFKVMQSKSKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	616
		GLCDNGKLKDALEMFK MQSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	676
		YEEMPHRGIVPDTITY+S+I GLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	559
Query	677	AGRVDDGLELFCMGRRGIVANAITYITL ICGFRKVGNGINGALDIFQEMISSGVYPDTIT	736
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFQEMMASGVYPDTIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY	766
		IRNMLTGLWSKEELKRAVAMLE LQMS+ Y	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSVGY	649

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESEAGFRGESLKLRSYSYEIK	60
Query	142	GLEDAIDLFSMDLRSLRPLPSVVDVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	201
		GLEDAIDLFSMDLRSLRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSMDLRSLRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120
Query	202	ILIKFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFET	261
		ILIKFCSCSKLPFALSTFGK+TKLGLHPDVVTFITLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKFCSCSKLPFALSTFGKLTKLGLHPDVVTFITLLHGLCLDHRVSEALDLFHQI---	177
Query	262	TCRPNVVTFITLLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	321
		CRP+V+TFITLLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDGMCCK GDTVSA	
Sbjct	178	-CRPDVLTFTLLMNGLCREGRVVEAVALDRMVENGLQPDQITYGTIVDGMCKMGDTVSA	236
Query	322	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIV	381
		LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	
Sbjct	237	LNLLRKMEEISHIKPNVVIYSAIIDGLCKDGRHSDSHNLFIEQDKGIFPNIVTYNCMIG	296

## Group 5

Query	382	GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	441
		GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	
Sbjct	297	GFCISGRWSAAQRLLEMLERKISPNVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSNLTITNTLIDGYCGAKRIDDGMELL	501
		NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCS++ TF TLIDGYCGAKRIDDGMELL	
Sbjct	357	NTITYNSMIDGFCKQDRDLAAEDMFYLMATKGCSPDVFTFTTLIDGYCGAKRIDDGMELL	416
Query	502	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLQEMISSGLCPDIVTCDTLLDGLCDN	561
		HEM GLVA+T TYNTLIHGF LVGDLNAAALDL Q+MISSG+CPDIVTC+TLDDGLCDN	
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	562	GKLKDALEMFKVMQKSKDLDASHPFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMP	621
		GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	
Sbjct	477	GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCKAGRVD	681
		HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMFVSMGSKSFSPNVVTFITTLINGYCKAGRVD	596
Query	682	DGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	741
		DGLELFCMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	
Sbjct	597	DGLELFCMGRRGIVADAIYITLIYGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEKLQMSMVY	766
		TG WSKEEL+RAVAMLE LQMS+ Y	
Sbjct	657	TGFWSKEELERAVAMLEDLQMSVGY	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Score = 1624 bits (4206), Expect = 0.0

Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGSSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
		MEAPNYPIFFGLNLGVPLEGGRSGTYSFGSSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	
Sbjct	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGSSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Query	61	LADSSRVFFRDRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
		LADSSRVFFRDRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	
Sbjct	61	LADSSRVFFRDRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPD	180
		SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPD	
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPD	180
Query	181	VISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLH	240
		VISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLH	
Sbjct	181	VISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLH	240

## Group 5

Query	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
		GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	
Sbjct	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQN L	360
		TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQN L	
Sbjct	301	TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQN L	360
Query	361	FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	420
		FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	
Sbjct	361	FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	420
Query	421	EGKFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLIT	480
		EGKFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLIT	
Sbjct	421	EGKFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLIT	480
Query	481	FNTLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMI	540
		FNTLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMI	
Sbjct	481	FNTLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMI	540
Query	541	SSGLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYN IL	600
		SSGLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYN IL	
Sbjct	541	SSGLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYN IL	600
Query	601	ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	660
		ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	
Sbjct	601	ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	660
Query	661	SPNVVTFTTLINGYCKAGRVDDGLELFCEMGRRGIVANAITYIT LICGFRKVG NINGALD	720
		SPNVVTFTTLINGYCKAGRVDDGLELFCEMGRRGIVANAITYIT LICGFRKVG NINGALD	
Sbjct	661	SPNVVTFTTLINGYCKAGRVDDGLELFCEMGRRGIVANAITYIT LICGFRKVG NINGALD	720
Query	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMS MVYYWSELKRHTFQKIS	780
		IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMS MVYYWSELKRHTFQKIS	
Sbjct	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMS MVYYWSELKRHTFQKIS	780
Query	781	GVKRCLGVCPFC SCHHGYRQARSS	804
		GVKRCLGVCPFC SCHHGYRQARSS	
Sbjct	781	GVKRCLGVCPFC SCHHGYRQARSS	804

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 6 from Brown provisional No. 2 (60/305,363)**

Score = 975 bits (2521), Expect = 0.0

Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRD TLA KASGESCEAGFGGESLKLQSGFHEIKGL	143
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRS GFHEIKGL	59

## Group 5

Query	144	EDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	203
Sbjct	60	EDAIDLFDMD+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	119
Query	204	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	263
Sbjct	120	+KCFCSCSKLPFALSTFGKITKLGLG-----FH-----	145
Query	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
Sbjct	146	P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+ -PTVVTFTSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA	200
Query	324	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	377
Sbjct	201	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ + LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	378	SMIVGFCSSGRWSDAEQQLQEMLERK-ISP DVVTYNALINAFVKEGKFFAEAEELYDEMLP	436
Sbjct	260	MI GFCSSGRWS+A+QQLQEMLERK ISP DVVTYNALINAFVKEGKFFAEAEELYDEMLP CMINGFCSSGRWSEAQQLQEMLERKKISP DVVTYNALINAFVKEGKFFAEAEELYDEMLP	319
Query	437	RGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	496
Sbjct	320	RGIIP+TITYSSMIDGFCQNRDLAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD RGIIPSTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPDIITFNTLIAGYCRARVDD	379
Query	497	GMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	556
Sbjct	380	G++LLHEMTE GLVA+T TY TLIHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD GIKLLHEMTEAGLVANTITYTTT LIHGFCQVGD LNAAQDLLQEMVSSGVC PNVTCTNLLD	439
Query	557	GLCDNGKCLKDALEMFKVMQSKSKDL DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	616
Sbjct	440	GLCDNGKCLKDALEMFK MQSKS D+DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL GLCDNGKCLKDALEMFKAMQSKSKMDIDASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTT LINGYCK	676
Sbjct	500	YEEMPHRGIVPDTITY+S+I GLCKQSR LDEATQMFDSMGSKSFSPNVVTFTT LINGYCK YEEMPHRGIVPDTITYNSVIHGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTT LINGYCK	559
Query	677	AGRVDDGLELFCMGRRGIVANAITYITL ICGFRKVG NINGALDIFQEMISSGVYPDTIT	736
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVG NINGALDIFQEM++SGVYPDTIT AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVG NINGALDIFQEMMASGVYPDTIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY	766
Sbjct	620	IRNMLTGLWSKEELKRAVAMLE LQMS+ Y IRNMLTGLWSKEELKRAVAMLEDLQMSVGY	649

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)**

Score = 523 bits (1346), Expect = 6e-146

Identities = 262/398 (65%), Positives = 313/398 (78%), Gaps = 1/398 (0%)

## Group 5

Query	371	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFAEEL	430
Sbjct	4	P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	431	YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYC	489
Sbjct	64	+M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	490	GAKRIDDMGEMELLHEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIV	549
Sbjct	124	+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV	183
Query	550	TCDTLLDGLCDNGKLKDALEMFKVMQKSKDLDAHPFNGVEPDVQTYNILISGLINEGK	609
Sbjct	184	TC+TLLDGLCD GKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYNILISGLINEGK TCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK	243
Query	610	FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFTT	669
Sbjct	244	FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT	303
Query	670	LINGYCKAGRVDGGLFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG	729
Sbjct	304	LI GYCKAG VDDGGLFCEMGRRGIVANAITYITLI GFRKVGNGING+LDIFQEMISSG LITGYCKAGMVDDGGLFCEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG	363
Query	730	VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYY 767	
Sbjct	364	VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSMV + VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVSF 401	

Score = 394 bits (1012), Expect = 3e-107

Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query	263	CRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSAL	322
Sbjct	2	C+PNVVTFTTLMNGLCREGR+VEAVALDRM+EDGLQ QITYGTIVDGMCK GDTVSAL CKPNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL	61
Query	323	NLLRKMEEVSHIIPNVVIYSAIIDLCKDGRHSDAQNLFTMQEKGIFPDFTYNSMIVG	382
Sbjct	62	NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING	121
Query	383	FCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN	442
Sbjct	122	FCSSG+WS+A++LLQEML RKISPDVVT++ LINA VKEG A++L EM+ G+ PN FCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN	181
Query	443	TITYSSMIDGFCKQNRLDAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA	491
Sbjct	182	+T ++++DG C + +L A MF M A G P++ T+N LI G VVTCTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE	241
Query	492	KRIDDMGEMELLHEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTC	551
Sbjct	242	+ + EL EM G+V DT TY+++I+G L+ A + M S P+IVT GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF	301

## Group 5

```

Query  552  DTLLDGLCDNGKCLKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFL  611
          +TL+ G C  G + D LE+F  M +          G+  +  TY  LI  G    G
Sbjct  302  NTLITGYCKAGMVDDGLELFCEMGR-----RGIVANAITYITLIRGFRKVGNNIN  350

Query  612  EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDMS  655
          + ++++EM  G+ PDTIT  +M+ GL  +  L  A  M  +  +
Sbjct  351  GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL  394

```

Score = 300 bits (767), Expect = 8e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

```

Query  230  PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTTCRPNVVTFTTLMNGLCREGRIVEAVAL  289
          P+VVTFTTTL++GLC E RV EA+      +M E  +PN +T+ T+++G+C+ G  V A+ L
Sbjct   4    PNVVTFTTLMNGLCREGRVVEAVALLD RMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  290  LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDS  348
          L +M E  ++P + Y  I+DG+ K G    A NL  +M++  I P++V YS +I+
Sbjct  64    LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF  122

Query  349  CKDGRHSDAQNLFTMQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLQEMLE-----  401
          C  G+ S+AQ L  EM  + I PD+ T++ +I      G  + A+ LLQEM+
Sbjct  123  CSSGKWSEARLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV  182

Query  402  -----RKISPDVVTYNALINAFVKEG  422
          + PDV TYN LI+  + EG
Sbjct  183  VTCNTLLDGLCDRGKCLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG  242

Query  423  KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFN  482
          KF EAEELY+EM  RGI+P+T+TYSSMI+G CKQ+RLD A  MF  M +K  SPN++TFN
Sbjct  243  KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDMSGKSFSPNIVTFN  302

Query  483  TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAALDLLQEMISS  542
          TLI GYC A  +DDG+EL  EM  G+VA+  TY TLI GF  VG++N +LD+ QEMISS
Sbjct  303  TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNNINGSLDIFQEMISS  362

Query  543  GLCPDIVTCDTLLDGLCDNGKCLKDALEMFKVMQKS  577
          G+ PD +T  +L GL  +LK AL M + +Q S
Sbjct  363  GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS  397

```

Score = 216 bits (551), Expect = 8e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

```

Query  160  PSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALST  219
          P+VV F  LM  + R  R    ++L  +M    ++ +  ++  ++  C      AL+
Sbjct   4    PNVVTFTTLMNGLCREGRVVEAVALLD RMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  220  FGKITKLG-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTTCRPNVVTFTTLMNGLC  278
          K+ +L  + PDVV ++ ++ GL  + R ++A + F +M +  P++VT++ ++NG C
Sbjct  64    LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC  123

```



## Group 5

Query	279	REGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LNLLRKMEEVSHIIPNV	338
		G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISP DVVTFSG LINALVKEGDLNSAQDLLQEMIS-SGVC PNV	182
Query	339	VIYSAIIDLCKDGRHSDAQNLFTMQE-----KGIFPDLFTYNSMIVGFCSSG	387
		V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G	
Sbjct	183	VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYN ILISGLINEG	242
Query	388	RWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIPNTITYS	447
		++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++	
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSR LDEATQMFDSMGSKSFSPNIVTFN	302
Query	448	SMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDMELLHEMTET	507
		++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +	
Sbjct	303	TLITGYCKAGMVDDGLELFC EMGRRGIVANAITYITLIRGFRKVG NINGS LDI FQEMISS	362
Query	508	GLVADTTTTYNTLIHGFYLVGDLNAA LLLQEM	539
		G+ DT T ++ G + +L AL +L+E+	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 193 bits (491), Expect = 8e-47

Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	145	DAIDLFS DMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMER-KQIRCDIYSFNIL	203
		+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +	
Sbjct	24	EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEELSHIKPDVVIYSAI	83
Query	204	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	263
		I + A + F ++ G+ PD+VT++ ++G C + SEA +M	
Sbjct	84	IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI	143
Query	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
		P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL	
Sbjct	144	SPDVVTFSG LINALVKEGDLNSAQDLLQEMISSGVC PNVVTCNTLLDGLCDRGKLDKDALE	203
Query	324	LLRKME-----EVSH----IIPNVVIYSAIIDLCKDGRHSDAQNLFTMQEKGIFPDL	373
		+ + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD	
Sbjct	204	MFKAMQKSMMDIDATHAFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHRGIVPDT	263
Query	374	FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEAEEELYDE	433
		TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E	
Sbjct	264	VTYSSMINGLCKQSR LDEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFC	323
Query	434	MLPRGIIPNTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR	493
		M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +	
Sbjct	324	MGRRGIVANAITYITLIRGFRKVG NINGS LDI FQEMISSGVYPDTITIRNMLTGLWSKEE	383
Query	494	IDDMELLHEM	504
		+ + +L E+	
Sbjct	384	LKRALAMLEEL	394

## Group 5

Score = 118 bits (296), Expect = 3e-24  
Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

```

Query 135 SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIR 194
          +GF      +A L +ML + P VV F L+ +V+ + L Q+M +
Sbjct 120 NGFCSSGKWSEAQRLLQEMLVRKISP DVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC 179

Query 195 CDIYSFNILIKFCSCSKLPFALSTFGKITKL-----GLHPDVVTF TLLHGLC 243
          ++ + N L+ C KL AL F + K G+ PDV T+ L+ GL
Sbjct 180 PNVVTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI 239

Query 244 VEDRVSEALDFFHQMFETTCTRPNVVTF TLMNGLCREGRIVEAVALLDRMMEDGLQPTQI 303
          E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +
Sbjct 240 NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIV 299

Query 304 TYGTIVDGMCKKGDTVSA LNLLRKMEEVSHIIPNVVIYSAIIDLCKDGRHSDAQNLFTE 363
          T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E
Sbjct 300 TFNTLITGYCKAGMVDDGLELFCCEMGRRG-IVANAITYITLIRGFRKVG NINGS LDIFQE 358

Query 364 MQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS 405
          M G++PD T +M+ G S A +L+E+ +S
Sbjct 359 MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS 400

```

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESEAGFRGESLKLRSYSYEIK	60
Query	142	GLEDAIDLFSMDLRSLRPLPSVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	201
		GLEDAIDLFSMDLRSLRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSMDLRSLRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120
Query	202	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFSTLLHGLCVEDRVSEALDFFHQMFET	261
		ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFSTLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFSTLLHGLCLDHRVSEALDLFHQI---	177
Query	262	TCRPNVVTFSTLLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	321
		CRP+V+TFSTLLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMCCK GDTVSA	
Sbjct	178	-CRPDVLTFTLLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGTFVDGMCKMGDTVSA	236

## Group 5

Query	322	LNLLRKMEEVSHIIPNVVIYSIAIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIV	381
Sbjct	237	LNLLRKMEE+SHI PNVVIYSIAID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	382	GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFCISGRWSAAQRLQEMLERKISPNVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL	501
Sbjct	357	NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL	416
Query	502	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTCDTLLDGLCDN	561
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	562	GKLKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP	621
Sbjct	477	GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTF TTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFVSMGSKSFSPNVVTFNTLINGYCKAGRVD	596
Query	682	DGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	741
Sbjct	597	DGLELFCCEMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEKLQMSMVY	766
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+ Y	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1624 bits (4206), Expect = 0.0

Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGGSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Sbjct	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGGSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Query	61	LADSSRVFFRDRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFRDRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120

## Group 5

Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD L	180
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD L	180
Query	181	VISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLH	240
Sbjct	181	VISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLH	240
Query	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Sbjct	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNL	360
Sbjct	301	TQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNL	360
Query	361	FTEMQEKGIFPD LFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	420
Sbjct	361	FTEMQEKGIFPD LFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVK	420
Query	421	EGKFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQNR LDAAEHMFYLMATKGCS PN LIT	480
Sbjct	421	EGKFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQNR LDAAEHMFYLMATKGCS PN LIT	480
Query	481	FNTLIDGYCGAKRID DGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMI	540
Sbjct	481	FNTLIDGYCGAKRID DGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMI	540
Query	541	SSGLCPDIVTCD TLLDGLCDNGKLDKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYN IL	600
Sbjct	541	SSGLCPDIVTCD TLLDGLCDNGKLDKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYN IL	600
Query	601	ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	660
Sbjct	601	ISGLINEGKFLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSF	660
Query	661	SPNVVTFTT LINGYCKAGRVD DGLELFCEMGRRGIVANAITYITL ICGFRKVG NINGALD	720
Sbjct	661	SPNVVTFTT LINGYCKAGRVD DGLELFCEMGRRGIVANAITYITL ICGFRKVG NINGALD	720
Query	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	780
Sbjct	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	780
Query	781	GVKRCLGVCPFC SCHHGYRQARSS	804
Sbjct	781	GVKRCLGVCPFC SCHHGYRQARSS	804

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)**

## Group 5

Score = 975 bits (2521), Expect = 0.0

Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	144	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	203
		EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVID FCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	204	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC	263
		+KCFCSKLPFALSTFGKITKLGLG FH	
Sbjct	120	MKCFCSKLPFALSTFGKITKLGLG-----FH-----	145
Query	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFTSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA	200
Query	324	LLRKMEEVSHIIPNVVIYSIAIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	377
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	378	SMIVGFCSSGRWSDAEQLLQEMLERK-ISPDPVTYNALINAFVKEGKFFAEELYDEMLP	436
		MI GFCSSGRWS+A+QLLQEMLERK ISPDPVTYNALINAFVKEGKFFAEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQQLLQEMLERKKISPDPVTYNALINAFVKEGKFFAEELYDEMLP	319
Query	437	RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	496
		RGIIP+TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD	379
Query	497	GMELLHEMTETGLVADTTTYNTLIHG FYLVDGLNAA DLLQEMISSGLCPDIVTCDTLLD	556
		G++LLHEMTE GLVA+T TY TLIHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHGFCQVGD LNAAQDLLQEMVSSGVC PNVVTCNTLLD	439
Query	557	GLCDNGKLKDALEMFKVMQSKSKDL DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	616
		GLCDNGKLKDALEMFK MQSK D+DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKSKMDIDASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	676
		YEEMPHRGIVPDTITY+S+I GLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	559
Query	677	AGRVDDGLELFCMGRRGIVANAITYITLIGFRKVG NINGALDIFQEMISSGVYPDTIT	736
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVG NINGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVG NINGALDIFQEMMASGVYPDTIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY	766
		IRNMLTGLWSKEELKRAVAMLE LQMS+ Y	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSVGY	649

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found



## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 521 bits (1341), Expect = 2e-145

Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query	288	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVITYNALINAFVKEGKFFAEEL	347
		P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	348	YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYC	406
		+M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	407	GAKRIDDGMELLHEMTETGLVADTTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIV	466
		+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISPDVVTFSGLLNALVKEGDLNSAQDLLQEMISSGVCPNVV	183
Query	467	TCDTLLDGLCDNGKLKDALEMFKVMQSKKDL DASHFNGVEPDVQTYNILISGLINEGK	526
		TC+TLLDGLCD GKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYNILISGLINEGK	
Sbjct	184	TCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK	243
Query	527	FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFTT	586
		FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T	
Sbjct	244	FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT	303

## Group 5

```

Query  587  LINGYCKAGRVDGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG  646
          LI  GYCKAG VDDGLELFCCEMGRRGIVANAITYITLI  GFRKVGNGING+LDIFQEMISSG
Sbjct   304  LITGYCKAGMVDDGLELFCCEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG  363

Query  647  VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM   681
          VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM
Sbjct   364  VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM   398

```

Score = 394 bits (1012), Expect = 2e-107  
Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

```

Query  180  CRPNVVTFTTLMNGLCREGRIVEAVALLDMMEDGLQPTQITYGTIVDGMCKKGDTVSA  239
          C+PNVVTFTTLMNGLCREGR+VEAVALLDMM+EDGLQP QITYGTIVDGMCK GDTVSA
Sbjct   2    CKPNVVTFTTLMNGLCREGRVVEAVALLDMMVEDGLQPNQITYGTIVDGMCKMGDTVSA  61

Query  240  NLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVG  299
          NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
Sbjct   62  NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING  121

Query  300  FCSSGRWSDAEQLLQEMLERKISPDPVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN  359
          FCSSG+WS+A++LLQEML RKISPDPVVT++ LINA VKEG A++L EM+ G+ PN
Sbjct   122  FCSSGKWSEAQRLLQEMLVKRISPDPVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN  181

Query  360  TITYSSMIDGFCKQNRDLAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA  408
          +T ++++DG C + +L A MF M A G P++ T+N LI G
Sbjct   182  VVTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE  241

Query  409  KRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTC  468
          + + EL EM G+V DT TY+++I+G L+ A + M S P+IVT
Sbjct   242  GKFLAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF  301

Query  469  DTLLDGLCDNGKLDKDALEMFKVMQKSKKDLDAHPFNGVEPDVQTYNILISGLINEGKFL  528
          +TL+ G C G + D LE+F M + G+ + TY LI G G
Sbjct   302  NTLITGYCKAGMVDDGLELFCCEMGR-----RGIVANAITYITLIRGFRKVGNGIN  350

Query  529  EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM  572
          + ++++EM G+ PDTIT +M+ GL + L A M + +
Sbjct   351  GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL  394

```

Score = 300 bits (767), Expect = 6e-79  
Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

```

Query  147  PDPVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCTRPNVVTFTTLMNGLCREGRIVEAVAL  206
          P+VVTFTTTL++GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L
Sbjct   4    PNVVTFTTLMNGLCREGRVVEAVALLDMMVEDGLQPNQITYGTIVDGMCKMGDTVSA  63

Query  207  LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSA  265
          L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
Sbjct   64  LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF  122

```

## Group 5

Query	266	CKDGRHSDAQNLFTTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLE-----	318
		C G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+	
Sbjct	123	CSSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPCNV	182
Query	319	-----RKISPDVVTYNALINAFVKEG	339
		+ PDV TYN LI+ + EG	
Sbjct	183	VTCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG	242
Query	340	KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFN	399
		KF EAEELY+EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN	
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN	302
Query	400	TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAAALDLLQEMISS	459
		TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS	
Sbjct	303	TLITGYCKAGMVDDGLELFCMGRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS	362
Query	460	GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS 494	
		G+ PD +T +L GL +LK AL M + +Q S	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS 397	

Score = 216 bits (551), Expect = 7e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query	77	PSVVDVFCCKLMGVVVRMERPDVISLYQKMERKQIRCDIYSFNILIKFCSCSKLPFALST	136
		P+VV F LM + R R ++L +M ++ + ++ ++ C AL+	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	137	FGKITKLG-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLC	195
		K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	196	REGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV	255
		G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV	
Sbjct	124	SSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPCNV	182
Query	256	VIYSAIIDLCKDGRHSDAQNLFTTEMQ-----KGIFPDLFTYNSMIVGFCSSG	304
		V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G	
Sbjct	183	VTCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG	242
Query	305	RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNTITYS	364
		++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++	
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN	302
Query	365	SMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHEMTET	424
		++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +	
Sbjct	303	TLITGYCKAGMVDDGLELFCMGRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS	362
Query	425	GLVADTTTYNTLIHGFYLVGDLNAAALDLLQEM 456	
		G+ DT T ++ G + +L AL +L+E+	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394	

## Group 5

Score = 193 bits (491), Expect = 6e-47  
Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	62	DAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL	120
		+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +	
Sbjct	24	EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAL	83
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFETTC	180
		I + A + F ++ G+ PD+VT++ +++G C + SEA +M	
Sbjct	84	IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI	143
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	240
		P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL	
Sbjct	144	SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNVTCTNTLLDGLCDRGKLDKDALE	203
Query	241	LLRKME-----EVSH----IIPNVVIYSALIDSCKDGRHSDAQNLFTMQEKGIFPDL	290
		+ + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD	
Sbjct	204	MFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHRGIVPDT	263
Query	291	FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFAEELYDE	350
		TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E	
Sbjct	264	VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCE	323
Query	351	MLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR	410
		M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +	
Sbjct	324	MGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE	383
Query	411	IDDGMELLHEM	421
		+ + +L E+	
Sbjct	384	LKRALAMLEEL	394

Score = 118 bits (296), Expect = 3e-24  
Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

Query	52	SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIR	111
		+GF +A L +ML + P VV F L+ +V+ + L Q+M +	
Sbjct	120	NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC	179
Query	112	CDIYSFNILIKCFCSCSKLPFALSTFGKITKL-----GLHPDVVTFITLLHGLC	160
		++ + N L+ C KL AL F + K G+ PDV T+ L+ GL	
Sbjct	180	PNVVTCTNTLLDGLCDRGKLDKDALEMFAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI	239
Query	161	VEDRVSEALDFFHQMFETTCTPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI	220
		E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +	
Sbjct	240	NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIV	299

## Group 5

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Query  221  TYGTIVDGMCKKGDTVSA LNLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNL FTE  280
          T+ T++ G CK G      L L  +M      I+ N + Y  +I      K G  + + ++F E
Sbjct  300  TFNTLITGYCKAGMVDDGLELFC EMGRRG-IVANAITYITLIRGFRKVG NINGS LDIFQE  358

Query  281  MQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS  322
          M  G++PD  T  +M+ G  S      A  +L+E+  +S
Sbjct  359  MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS  400

```

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSGSYEIK	60
Query	59	GLEDAIDLFSDDLRSRPLPSVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	118
		GLEDAIDLFSDDLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSDDLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120
Query	119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFET	178
		ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFITLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFITLLHGLCLDHRVSEALDLFHQI---	177
Query	179	TCRPNVVTFITLLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
		CRP+V+TFITLLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDGMCCK GDTVSA	
Sbjct	178	-CRPDVLTFTITLLMNGLCREGRVVEAVALDRMVENGLQPDQITYGTIVDGMCKMGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIV	298
		LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	
Sbjct	237	LNLLRKMEEISHIKPNVVIYSAIIDGLCKDGRHSDSHNLFIEQMKGIFPNIVTYNCMIG	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	358
		GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	
Sbjct	297	GFCISGRWSAAQRLQLQEMLERKISPNVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSNLTITNTLIDGYCGAKRIDDGMELL	418
		NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCS++ TF TLIDGYCGAKRIDDGMELL	
Sbjct	357	NTITYNSMIDGFCKQDRDLAAEDMFYLMATKGCSPDVFTITNTLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTCDTLLDGLCDN	478
		HEM GLVA+T TYNTLIHGF LVGDLNAAALDL Q+MISSG+CPDIVTC+TLLDGLCDN	
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	479	GKLKDALEMFKVMQKSKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP	538
		GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	
Sbjct	477	GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCKAGRVD	598
		HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMFVSMGSKSFSPNVVTFNTLINGYCKAGRVD	596
Query	599	DGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	658
		DGLELFCMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	
Sbjct	597	DGLELFCMGRRGIVADAIYITLIYGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656

## Group 5

Query 659 TGLWSKEELKRAVAMLEKLQMSM 681  
 TG WSKEEL+RAVAMLE LQMS+  
 Sbjct 657 TGFWSKEELERAVAMLEDLQMSV 679

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1368 bits (3541), Expect = 0.0

Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	
Sbjct	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	
Sbjct	144	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCKLPPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
		IKCFCSCKLPPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	
Sbjct	204	IKCFCSCKLPPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	300
		LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	
Sbjct	324	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
		CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	
Sbjct	384	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCS PNLITFNTLIDGYCGAKRIDDGMELLHE	420
		ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCS PNLITFNTLIDGYCGAKRIDDGMELLHE	
Sbjct	444	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCS PNLITFNTLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
		MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	
Sbjct	504	MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
		LKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	
Sbjct	564	LKDALEMFKVMQSKKDL DASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623



## Group 5

Query	541	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCKAGRVDG	600
		GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCKAGRVDG	
Sbjct	624	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCKAGRVDG	683
Query	601	LELFCEMGRRGIVANAITYITLICGFRKVGNGALDIFQEMISSGVYPDTITIRNMLTG	660
		LELFCEMGRRGIVANAITYITLICGFRKVGNGALDIFQEMISSGVYPDTITIRNMLTG	
Sbjct	684	LELFCEMGRRGIVANAITYITLICGFRKVGNGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
		LWSKEELKRAVAMLEKLQMSM	
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)**

Score = 974 bits (2517), Expect = 0.0  
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	61	EDAIDLFSDMLRSRPLPSVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVIDFCKLMGVVVRMGRDLVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSKLPFALSTFGKITKLG FH	
Sbjct	120	MKCFCSCSKLPFALSTFGKITKLG-----FH-----	145
Query	181	RPNVVTFITLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFITLLHGLCVEDRISEALDLFHQMCK----PNVVTFITLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	294
		LL +M E + PN + Y I+D+CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLLQEMLERK-ISP DVVTYNALINAFVKEGKFFEAEELYDEMLP	353
		MI GFCSSGRWS+A+QLLQEMLERK ISP DVVTYNALINAFVKEGKFFEAEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQQLLQEMLERKKISP DVVTYNALINAFVKEGKFFEAEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	413
		RGIIP+TITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD	379
Query	414	GMELLHEMTETGLVADTTTYNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	473
		G++LLHEMTE GLVA+T TY TLIHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTT LIHGFCQVGD LNAAQDLLQEMVSSGVC PNVT CNTLLD	439

## Group 5

Query	474	GLCDNGKLKDALEMFKVMQSKSKDL DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQSKS D+DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKSKMDIDASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTF TT LINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEATQMFDSMGSKSFSPNVVTF TT LINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDSMGSKSFSPNVVTF TT LINGYCK	559
Query	594	AGRVDDGLELFCEMGRRGIVANAITYITLICGFRKVG NINGALDIFQEMISSGVYPDTIT	653
		AGRVDDGLELFCEMGRRGIVANAITYITLI GFRKVG NINGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCEMGRRGIVANAITYITLIHGFRKVG NINGALDIFQEMMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM	681
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV	647

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSYSYEIK	60
Query	59	GLEDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	118
		GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSDMLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120

## Group 5

Query	119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVFTFTLLHGLCVEDRVSEALDFFHQMFET	178
Sbjct	121	ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVFTFTLLHGLC++ RVSEALD FHQ+	177
Query	179	TCRPNVVFTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
Sbjct	178	-CRPDVLTFTTLMNGLCREGRVVEAVALDRMVENGLQPDQITYGTIVDGMCKMGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIV	298
Sbjct	237	LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	299	GFCSSGRWSDAEQLQEMLERKISPVDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	358
Sbjct	297	GFCISGRWSAAQRLQEMLERKISPVDVVTYNALINAFVKEGKFFEA EEELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSNPNTITFNTLIDGYCGAKRIDDGMELL	418
Sbjct	357	NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCS++ TF TLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTCDTLLDGLCDN	478
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	479	GKLKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMP	538
Sbjct	477	GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVFTFTTLINGYCKAGRVD	598
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	596
Query	599	DGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	658
Sbjct	597	DGLELFCCEMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM	681
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+	679

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Score = 1368 bits (3541), Expect = 0.0

Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
Sbjct	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143

## Group 5

Query	61	EDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCKSLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCKSLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
Query	241	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNR LDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELLHE	420
Sbjct	444	ITYSSMIDGFCKQNR LDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTF TT LINGYCKAGRVD DG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTF TT LINGYCKAGRVD DG	683
Query	601	LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVYPDTITIRNMLTG	660
Sbjct	684	LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against SEQ 6 from Brown provisional No. 2 (60/305,363)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

## Group 5

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
Sbjct	1	MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
Sbjct	60	EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVID FCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct	120	+KCFCSKLPFALSTFGKITKLGL FH	
Sbjct	120	MKCFCSKLPFALSTFGKITKLGL-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
Sbjct	146	P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+ -PTVVTFSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYS AIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	294
Sbjct	201	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ + LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLLQEMLERK-ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	353
Sbjct	260	MI GFCSSGRWS+A+QLLQEMLERK ISP DVVTYNALINAFVKEGKFFAEELYDEMLP CMINGFCSSGRWSEAQQLLQEMLERKKISP DVVTYNALINAFVKEGKFFAEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	413
Sbjct	320	RGIIP+TITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD RGIIPSTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPIITFNTLIAGYCRAKRVDD	379
Query	414	GMELLHEMTETGLVADTTTNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	473
Sbjct	380	G++LLHEMTE GLVA+T TY TLIHGF VGDLNAA DLLQEM+SSG+CP++VTC+TLLD GIKLLHEMTEAGLVANTITYTTLIHGFCQVGDLNAAQDLLQEMVSSGVC PNVT CNTLLD	439
Query	474	GLCDNGKLKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	533
Sbjct	440	GLCDNGKLKDALEMFK MQSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	593
Sbjct	500	YEEMPHRGIVPDTITY+S+I GLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK YEEMPHRGIVPDTITYNSVIHGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	559
Query	594	AGRVDDGLELFCMGRRGIVANAITYITL ICGFRKVGNGINGALDIFQEMISSGVYPDTIT	653
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFQEM++SGVYPDTIT AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFQEMMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM	681
Sbjct	620	IRNMLTGLWSKEELKRAVAMLE LQMS+ IRNMLTGLWSKEELKRAVAMLEDLQMSV	647

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)**

## Group 5

Score = 521 bits (1341), Expect = 2e-145

Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query	288	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDRVVTYNALINAFVKEGKFFAEEL	347
		P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	348	YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPLNLTFTNLIDGYC	406
		+M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	407	GAKRIDDGMELLHEMTETGLVADTTTTYNTLIHGFIYLVGDLNAAALDLLQEMISSGLCPDIV	466
		+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISPDRVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV	183
Query	467	TCDTLLDGLCDNGKLKDALEMFKVMQKSKDLDAHPFNGVEPDVQTYNIIISGLINEGK	526
		TC+TLLDGLCD GKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYNIIISGLINEGK	
Sbjct	184	TCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGK	243
Query	527	FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFTT	586
		FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T	
Sbjct	244	FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT	303
Query	587	LINGYCKAGRVDGGLFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG	646
		LI GYCKAG VDDGGLFCEMGRRGIVANAITYITLI GFRKVGNGING+LDIFQEMISSG	
Sbjct	304	LITGYCKAGMVDDGGLFCEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG	363
Query	647	VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM	681
		VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM	
Sbjct	364	VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM	398

Score = 394 bits (1012), Expect = 2e-107

Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query	180	CRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSAL	239
		C+PNVVTFTTLMNGLCREGR+VEAVALDRM+EDGLQP QITYGTIVDGMCK GDTVSAL	
Sbjct	2	CKPNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL	61
Query	240	NLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTMQEKGIFPDFTYNSMIVG	299
		NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G	
Sbjct	62	NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING	121
Query	300	FCSSGRWSDAEQLLQEMLERKISPDRVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN	359
		FCSSG+WS+A++LLQEML RKISPDRVVT++ LINA VKEG A++L EM+ G+ PN	
Sbjct	122	FCSSGKWSEAQRLLQEMLVRKISPDRVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN	181
Query	360	TITYSSMIDGFCKQNRLDAAEHMFYLM-----ATKGCSPLNLTFTNLIDGYCGA	408
		+T ++++DG C + +L A MF M A G P++ T+N LI G	
Sbjct	182	VVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINE	241

## Group 5

```

Query  409  KRIDDGMELLHEMTETGLVADTTTNTLIHGFYLVGDLNAAALDLLQEMISSGLCPDIVTC  468
          +  +  EL  EM   G+V DT TY+++I+G      L+ A  +   M S   P+IVT
Sbjct  242  GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF  301

Query  469  DTLLDGLCDNGKLKDALEMFKVMQKSKKDL DASHFNGVEPDVQTYNILISGLINEGKFL  528
          +TL+ G C   G + D LE+F  M +              G+  +  TY  LI G   G
Sbjct  302  NTLITGYCKAGMVDDGLELFCEMGR-----RGIVANAITYITLIRGFRKVGNNIN  350

Query  529  EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM  572
          + ++++EM   G+ PDTIT  +M+ GL  +  L  A  M  +  +
Sbjct  351  GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL  394

```

Score = 300 bits (767), Expect = 6e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

```

Query  147  PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVAL  206
          P+VVTFTTL++GLC E RV EA+      +M E   +PN +T+ T+++G+C+ G   V A+ L
Sbjct   4   PNVVTFTTLMNGLCREGRVVEAVAL LDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  207  LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDL  265
          L +M E   ++P  + Y  I+DG+ K G   A NL  +M++   I P++V YS +I+
Sbjct  64   LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF  122

Query  266  CKDGRHSDAQNLFTTEMQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLQEMLE-----  318
          C  G+ S+AQ L  EM  + I PD+ T++ +I      G  + A+ LLQEM+
Sbjct  123  CSSGKWSEAQRL LQEMLV RKISP DVVTF SGLINALVKEGDLNSAQDLLQEMISSGVCPNV  182

Query  319  -----RKISP DVVTYNALINAFVKEG  339
          + PDV TYN LI+  + EG
Sbjct  183  VTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG  242

Query  340  KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQNRLDAAEHMFYLMATKGCSPNLITFN  399
          KF EAEELY+EM  RGI+P+T+TYSSMI+G CKQ+RLD A  MF  M +K  SPN++TFN
Sbjct  243  KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN  302

Query  400  TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTNTLIHGFYLVGDLNAAALDLLQEMISS  459
          TLI GYC A  +DDG+EL  EM   G+VA+  TY TLI GF  VG++N +LD+ QEMISS
Sbjct  303  TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNNINGSGLDIFQEMISS  362

Query  460  GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS  494
          G+ PD +T   +L GL   +LK AL M  + +Q S
Sbjct  363  GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS  397

```

Score = 216 bits (551), Expect = 7e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)



## Group 5

Query	77	PSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST	136
		P+VV F LM + R R ++L +M ++ + ++ ++ C AL+	
Sbjct	4	PNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSA LN	63
Query	137	FGKITKL G-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLC	195
		K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	
Sbjct	64	LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC	123
Query	196	REGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LNLLRKMEEVSHIIPNV	255
		G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV	
Sbjct	124	SSGKWSEAQRLLQEMLVRKISP DVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVC PNV	182
Query	256	VIYSAIIDLCKDGRHSDAQNLFTMQE-----KGIFPD LFTYNSMIVGFCSSG	304
		V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G	
Sbjct	183	VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYN ILISGLINEG	242
Query	305	RWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIPNTITYS	364
		++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++	
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSR LDEATQMFDSMGSKSFSPNIVTFN	302
Query	365	SMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDMELLHEMTET	424
		++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +	
Sbjct	303	TLITGYCKAGMVDDGLELFC EMGRRGIVANAITYITLIRGFRKVG NINGSLSLDIFQEMISS	362
Query	425	GLVADTTTYNTLIHGFYLVGDLNAALDLLQEM	456
		G+ DT T ++ G + +L AL +L+E+	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 193 bits (491), Expect = 6e-47

Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	62	DAIDLFS DMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMER-KQIRCDIYSFNIL	120
		+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +	
Sbjct	24	EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSA LNLLRKMEELSHIKPDVVIYSAI	83
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC	180
		I + A + F ++ G+ PD+VT++ +++G C + SEA +M	
Sbjct	84	IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI	143
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL	
Sbjct	144	SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC PNVVTCNTLLDGLCDRGKLDKDALE	203
Query	241	LLRKME-----EVSH----IIPNVVIYSAIIDLCKDGRHSDAQNLFTMQEKGIFPD L	290
		+ + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD	
Sbjct	204	MFKAMQKSMMDIDATHAFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHRGIVPDT	263
Query	291	FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFFEAEEELYDE	350
		TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E	
Sbjct	264	VTYSSMINGLCKQSR LDEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFC	323

## Group 5

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Query 351 MLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPLITFNTLIDGYCGAKR 410
          M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +
Sbjct 324 MGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE 383

Query 411 IDGGMELLHEM 421
          + + +L E+
Sbjct 384 LKRALAMLEEL 394

```

Score = 118 bits (296), Expect = 3e-24  
Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

```

Query 52 SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPDLVISLYQKMERKQIR 111
          +GF +A L +ML + P VV F L+ +V+ + L Q+M +
Sbjct 120 NGFCSSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC 179

Query 112 CDIYSFNILIKFCSCSKLPFALSTFGKITKL-----GLHPDVVTFITLLHGLC 160
          ++ + N L+ C KL AL F + K G+ PDV T+ L+ GL
Sbjct 180 PNVVTCNTLLDGLCDRGKLDKALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLI 239

Query 161 VEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI 220
          E + EA + + +M P+ VT++++NGLC++ R+ EA + D M P +
Sbjct 240 NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIV 299

Query 221 TYGTIVDGMCKKGDTVSAIINLLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNL FTE 280
          T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E
Sbjct 300 TFNTLITGYCKAGMVDDGLELFCCEMGRRG-IVANAITYITLIRGFRKVGNGSLDIFQE 358

Query 281 MQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS 322
          M G++PD T +M+ G S A +L+E+ +S
Sbjct 359 MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS 400

```

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCRFESSSSSSVSAARFFCTGSIRHALAEKSRDGESEAGFRGESLKLRSYSYEIK	60
Query	59	GLEDAIDLFSMDLRSRPLPSVVDVCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN	118
		GLEDAIDLFSMDLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSMDLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT	120
Query	119	ILIKCFCSCKLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFET	178
		ILIKCFCSCKLPFALSTFGK+TKLGLHPDVVTFITLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKCFCSCKLPFALSTFGKLTKLGLHPDVVTFITLLHGLCLDHRVSEALDLFHQI---	177

## Group 5

Query	179	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
		CRP+V+TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMCCK GDTVSA	
Sbjct	178	-CRPDVLTFTTLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGT FVDGMCKMGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSIAIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIV	298
		LNLLRKMEE+SHI PNVVIYSIAID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	
Sbjct	237	LNLLRKMEEISHIKPNVVIYSIAIDGLCKDGRHSDSHNLFIEMQDKGIFPNIVTYNCMIG	296
Query	299	GFCSSGRWSDAEQLQEMLERKISPVDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	358
		GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	
Sbjct	297	GFCISGRWSAAQRLLQEMLERKISPVDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL	418
		NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL	
Sbjct	357	NTITYNSMIDGFCKQDRDLAAEDMFYLMATKGCSPDVFTFTTLLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDN	478
		HEM GLVA+T TYNTLIHGF LVGDLNAALDL Q+MISSG+CPDIVTC+TLLDGLCDN	
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDLNAALDLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	479	GKLKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMP	538
		GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	
Sbjct	477	GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD	598
		HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMFVSMGSKSFSPNVVTFNTLINGYCKAGRVD	596
Query	599	DGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	658
		DGLELFCMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	
Sbjct	597	DGLELFCMGRRGIVADAIYITLIYGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM 681	
		TG WSKEEL+RAVAMLE LQMS+	
Sbjct	657	TGFWSKEELERAVAMLEDLQMSV 679	

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1368 bits (3541), Expect = 0.0

Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	
Sbjct	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143

## Group 5

Query	61	EDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCKSLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCKSLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	323
Query	241	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIPNVVIYS AIIDSLCKDGRHSDAQNLFTMQEKGIFPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFEEAEELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLQEMLERKISP DVVTYNALINAFVKEGKFEEAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNR LDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELLHE	420
Sbjct	444	ITYSSMIDGFCKQNR LDAAEHMFYLMATKGCS PN LITFNTLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTYNTLIHGFYLVGDLNAA LDLLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQKSKKDL DASHPFNGVEPDVQTYN ILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTF TT LINGYCKAGRVD DG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSR LDEATQMFD SMGSKSFSPNVVTF TT LINGYCKAGRVD DG	683
Query	601	LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVYPDTITIRNMLTG	660
Sbjct	684	LELFCEMGRRGIVANAITYIT LICGFRKVG NINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

## Group 5

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	61	EDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPD LVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVID FCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF TTLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSKLPFALSTFGKITKLGL FH	
Sbjct	120	MKCFCSKLPFALSTFGKITKLGL-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA LN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTMQEKG-IFPDLFTY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGGDTVSA LNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLLQEMLERK-ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	353
		MI GFCSSGRWS+A+QLLQEMLERK ISP DVVTYNALINAFVKEGKFFAEELYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQQLLQEMLERKKISP DVVTYNALINAFVKEGKFFAEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD	413
		RGIIP+TITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNR LDAAEHMFYLMATKGCSPIITFNTLIAGYCRAKRVDD	379
Query	414	GMELLHEMTETGLVADTTTNTLIHG FYLVGDLNAA DLLQEMISSGLCPDIVTCDTLLD	473
		G++LLHEMTE GLVA+T TY TLIHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHGFCQVGD LNAAQDLLQEMVSSGVC PNVT CNTLLD	439
Query	474	GLCDNGKLKDALEMFKVMQSKKDL DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQSK D+DASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHFPNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSR LDEATQMFDSMGSKSFSPNVVTFTTLINGYCK	559
Query	594	AGRVDDGLELFCMGRRGIVANAITYITL ICGFRKVGNGINGALDIFQEMISSGVYPDTIT	653
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFQEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFQEMMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM	681
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV	647

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)**

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found



## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found